

GenCore version 4.5						
copyright (c) 1993 - 2000	Query	No.	Score	Match	Length	DB ID
Compugen Ltd.						
OM nucleic - nucleic search, using sw model						
Run on: January 15, 2002, 17:31:55 ; search time 1398.01 seconds						
(without alignments)						
8543.543 Million cell updates/sec						
Title: US-09-762-633-3	Perfect score: 724	Sequence: 1 gaagtgttacaagaatggcc.....gatgtgttatggaaatgttaca	IDENTITY-NUC	Gapop 10.0 , Gapext 1.0	8248589755 residues	
Scoring table: 1472140 seqs, 8248589755 residues						
Searched: Total number of hits satisfying chosen parameters: 2944280						
Minimum DB seq length: 0						
Maximum DB seq length: 200000000						
Post-processing: Minimum Match 0%						
Maximum Match 100%						
Database: Listing first 45 summaries						
1: GenEmbl:*						
2: gb_ba:*						
3: gb_btg:*						
4: gb_cm:*						
5: gb_ov:*						
6: gb_pat:*						
7: gb_ph:*						
8: gb_pl:*						
9: gb_pr:*						
10: gb_ro:*						
11: gb_ss:*						
12: gb_sv:*						
13: gb_uni:*						
14: gb_vt:*						
15: em_ba:*						
16: em_fun:*						
17: em_hum:*						
18: em_in:*						
19: em_om:*						
20: em_ov:*						
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22: em_pat:*						
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24: em_pl:*						
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26: em_sts:*						
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28: em_un:*						
29: em_vt:*						
30: em_btgo_hum:*						
31: em_btgo_inv:*						
32: em_btgo_rnd:*						
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34: em_btg_inv:*						
35: em_btg_rnd:*						
36: em_btg_other:*						
ALIGNMENTS						
RESULT 1	AB022061	LOCUS	AB022061	724 bp	DNA	
DEFINITION	Pectinatus cerevisiphilus DNA, 16S/23S rRNA intergenic spacer				BCT	30-MAR-2000
ACCESSION	AB022061	REGION				
VERSION	AB022061.1	KEYWORDS	GI:7288087			
SOURCE	Pectinatus cerevisiphilus (strain:DSM4067) DNA.	ORGANISM				
AUTHORS	Motoyama, Y. and Ogata, T.					
TITLE	16S-23S rRNA spacer of Pectinatus, Selenomonas and Zymophilus reveal new phylogenetic relationships between these genera					
JOURNAL	Int. J. Syst. Evol. Microbiol.					
MEDLINE	20022199					
REFERENCE	2 (bases 1 to 724)					
AUTHORS	Ogata, T. and Motoyama, Y.					

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gene FIGKILKLERMHSAHRRKILLCVYASILGTTSHSLNKLNFNF¹
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 /codon_start=1
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 /note="CJ0344, unknown, len: 41 aa, no Hs match"
 /translation="MFQNITKYKDFIFIILNLKQNYLLTKINLQDFKNEHKSLNF"
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 1299. . 2549
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 /note="CJ0345, trpE, possible antranilate synthase component I, len: 416 aa, similar in C-terminal half to many e.g. TRPE_CLOM antranilate synthase component I (EC 4.1.3.27) (494 aa), fasta scores: opt: 784 z-score: 1209.9 E(0): 0, 47.0% identity in 281 aa overlap, 35.6% identity in 365 aa overlap to HP1282. Contains Pfam match to entry PF00425 chorismate bind chorismate binding enzyme, score 309.50, E-value 3.9e-89,
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 /translation="MFVNNDVNYRQOLEKFENSYFAEDLTQKVIIGDQDYLADANELS
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 YLYVEKNSRMMFKRKGASKYFEYKLUKDIEPMKKKKKNDPELNLSEDEKNDFLKACERA
 KYYLSSGDFIOWVKOLCIKADYEDVTESSLNPSATMYPSPKGWVGLSSPE
 FLKTKKREYLAPLAGTRNLNECDLIALEKOLLSLDSKNEHMKVMDLARNDASKP
 GTQPRVENEFLIKKFKVHYMEVSYVANMKEDASIDVDEIAVEFVPGTSLGAKTRALE
 ITSELEDDCGRYGGKFLNENEDDTILALTRCAFFTQDKAYLASGAGIVLQSESQK
 FVAEIACKRKKALLVAFENLKKENQ"
 1743. . 2522
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 2546. . 3103
 /gene="trpD"
 /note="Pfam match to entry PF00117 Gtase, Glutamine amidotransferases class-I, score 252.00, E-value 8.4e-72"
 2546. . 4147
 /gene="trpD"
 /EC_number="4.1.3.27"
 /note="CJ0346, trpD (trpGD), probable antranilate synthase component II, len: 533 aa, (contains glutamine amidotransferase and antranilate phosphoribosyltransferase) similar to many e.g. TRP_G_ECOLI antranilate synthase component II (EC 4.1.3.27) (530 aa), fasta scores: opt: 866 z-score: 781.3 E(0): 0, 32.6% identity in 528 aa overlap. N terminus has 34.6% identity to HP1281, C-terminus is 33.2% identity to HP1280. Contains PS00442 Glutamine amidotransferases class-I active site and Pfam matches to entry PF00117 Gtase, Glutamine amidotransferases class-I, score 252.00, E-value 8.4e-72 and to entry PF00591 Glycos_transf_3, glycosyl transferase family, score 138.60, E-value 1.1e-37,
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 PTHILSPGKHPQPGQGICLIEPKARLNIPVLGICLGHQALALAFDSVYKMOPEMHA
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 YVGQFHPESYFSYGLQLFSNEFLRQDKKPOQENPFLSKMSEHNFQDFDQ"
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 gene CDS
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 4134. . 4733
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 /EC_number="5.3.1.24"
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 4143. . 4721
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 /note="Pfam match to entry PF00697 PRAI, N-(5'-phosphoribosyl)anthranilate (PRA) isomerase, score 102.30, E-value 9.5e-27,"
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 /gene="trpB"
 4730. . 5908
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 KTKTEATTAAIOWGQDQKNNYVWSSAAGVYPPWVHQSICRECKMOLQKLN
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LEMKKVVITATSENFTNSNKGDSKDKFMEKRYNCDVLLDDQFLGKTDQLOE

FFFNFNETRKNDQIITMSDNPNNMLGKITERLSPRAGTIAIDTPPQLETKLIR

KKEFENDINLSDIINVYATSIGNDIREJGILISNAYATLGQBLTELEAKSMKD

HNEKENITIDDLSLVCKENIKPSDVKNKTONIVTARRYTYLAKALTALTMP

OLANYFEKRDHTAISHNVKKITEMIENDASLAKAKIEELKLNKILVKSQS"

301..11239

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/note="Pram match to entry PF00308 bac.dna, Bacterial

dna Protein, score 419.90, E-value 4e-141"

427..450

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/note="PS00117 ATP/GTP-binding site motif A (P-loop)"

1483..2535

/gene="dnan"

/note="Pram match to entry PF00712 DNA_Pol3_beta, DNA

polymerase III beta subunit, score 119.80, E-value

5.2e-32"

1483..2550

/gene="dnan"

/note="CJ0002_dnaN"

/EC_number="2.7.7.7"

/product="CJ0002_dnaN, Probable DNA polymerase III, beta

chain, len: 355 aa; similar to e.g. DPB_ECOLI DNA

polymerase III, beta chain (EC 2.7.7.7) (366 aa), fasta

scores; opt: 372.3 z-score: 1.7e-13, 19.6%

Identity in 367 aa overlap. 34.2% identity to HP0500.

Contains Pram match to entry PF00712 DNA_Pol3_beta, DNA

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5.2e-32"

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/translation="MKLINNNTLESAVILCNAVEKKDSSTITHLFFHADEDKLII

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TKYKUPMNEDEPNEPTEGKNOFDSSDLRSKILPSPDSDNNPKYSNAGFLD

ITDKDNFQDIDKRLAITLETEKANNOFSISPKAKMEMOKFLYKIEFQDNML

IAKNNENEFITPKLNDKPDYKQPKFQKSFSDFISLKKSVWKEKMLHF

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2579..4888

/gene="gyrB"

/note="5.99.1.3"

/EC_number="5.99.1.3"

/note="CJ0003_gyrB, probable DNA gyrase subunit B, len:

769 aa; similar to many e.g. GYR_BACSU DNA gyrase subunit

B (EC 5.99.1.3) (638 aa), fasta scores; opt: 2130 z-score:

3165.8 E()..0..47..7% identity in 773 aa overlap. 61.2%

identity to HP0501. Contains PS0017 DNA topoisomerase II

signature and Pram matches to entry PF00704 DNA_topoisom.

DNA_topoisomerase II (N-terminal region), score 915.20,

E-value 1.9e-271, and to entry PF0086 DNA_gyraseB_C, DNA

gyrase B subunit, carboxyl terminus, score 154.00, E-value

2.6e-42"

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KCTTIEFWPDQIFEFERDEILAKRFRERLWLNPKLTFNFKDNRKVFHFFEG

GISOFVFDLNLKREALKAIEFSDDEDVWVALLYNDYNSLISVWNIKPDGTT

HEAGFRMGLTRVSNTEANASAREDKNITGDDVREGLIAVSVKVPQFBBGQTK

/product="chromosomal replication initiator protein"

CJ1168X1..CJ1168X1 314150 bp DNA BCT 08-JUL-2000

/DEFINITION Camylobacter jejuni NCTC1168 complete genome; segment 1/6.

/ACCESSION AL139074 AL11168

/VERSION AL139074..2 GI:6967505

/KEYWORDS Campylobacter; *Campylobacter jejuni*.

/REFERENCE Authors: Jaelens, K., Karlyshev, A., Moulis, S., Pallen, M.J., Penn, C.W., Quail, M., Ralbandre, M.A., Rutherford, K.M., VanVliet, A., Whitehead, S. and Barrall, I.B.,

Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals 403 hypervariable sequences

Journal: Nature 403 (6770), 665-668 (2000)

Reference: Parkhill, J., Wren, B.W., Mungall, K., Ketley, J.M., Churcher, C., Basham, D., Chillingworth, T., Davies, R.M., Feltwell, T., Holroyd, S., Quail, M., Ralbandre, M.A., Rutherford, K.M., VanVliet, A., Whitehead, S. and Barrall, I.B.,

Author: Parkhill, J.

Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals 403 hypervariable sequences

Nature 403 (6770), 665-668 (2000)

20150912..20150912

/COMMENT Submitted on behalf of the *Campylobacter* sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhillsanger.ac.uk/COMMENT Details of *C. jejuni* sequencing at the Sanger Centre are available on the World Wide Web.(URL, http://www.sanger.ac.uk/projects/C_jejuni/).

/FEATURES source

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/FEATURES source

/COMMENT Details of *C. jejuni* sequencing


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361..768
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aa; similar to hypothetical proteins e.g. YJF_ECOLJ (153
aa), fasta scores: opt: 164 z-score: 205.3 E(): 0, 0.00339
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Contains PS0017 ATP/GTP-binding site motif A (P-loop)".
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protein, len: 242 aa; highly similar to many e.g.
YHBC_ECOLI Probable ABC transporter ATP-binding protein
(240 aa), fasta scores: opt: 840 z-score: 1144.2 E(): 0,
54.2% identity in 236 aa overlap. 65.8% identity to
HP015. Contains PS0017 ATP /GTP-binding site motif A
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845..1396
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<note="Pfam match to entry PF00005 ABC_tran, ABC
transporters, score 221.60, E-value 1.1e-62"
866..889
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1486..2718
<note="Pfam match to entry PF00309 Sigma54_factor"
Sigma54 factors family, score 42.30, E-value 8.4e-20"
1489..2739
<gene="rp0N"
<note="Cj0670, rp0N, probable RNA polymerase sigma-54
factor, len: 416 aa; similar to many e.g. RP54_BACSU RNA
polymerase sigma-54 factor (436 aa), fasta scores: opt:
357 z-score: 603.0 E(): 2.7e-26, 28.9% identity in 443 aa
overlap, and RP54_ECOLI (477 aa), fasta scores: opt: 365
z-score: 483.2 E(): 1.3e-19, 28.8% identity in 459 aa
overlap. 47.4% identity to HP0714. Contains PS00178
Sigma-54 factors family signature 2, Pfam match to entry
PF00349 Sigma54 factors, and helix-turn-helix motif at aa
301..324 (Score 1.227; +3.37 SD)".
<codon_start=1
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SOELARK1IECINEGCFEHDIFKEYSLEIERRARKEFLDGVGAKKDYKAFL
I1VPDIFVYKNGEYKVKINDYDYPISIOTDGLBHDLSHYKEANLVDALMKA
LYK1GMLIVYEVYOFWGMGEK1KPFMDAIDLERNASISRAVANK1LSCRGCLP
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<note="PS00178 Sigma-54 factors family signature 2".
2903..4327
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<note="dcuB"
<gene="Cj0671 dcuB, probable anaerobic C4-dicarboxylate
transporter, len: 474 aa; highly similar to e.g.
DCUB_ECOLI anaerobic C4-dicarboxylate transporter
a opt: 1280 z-score: 2918.6 E(): 0, 69.1% identity in 466
aa overlap. No HP ortholog. Also similar to Cj0088, dcuA
(37.0% identity in 465 aa overlap)".
<codon_start=1
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AVSLSLTALNNHAKLQFDGYVNLQLOTIPFLGVLCTGFSWFGKDDKDEVQF
EK1KDPERKKVYVGDSKTLGLYKLPKSWWWAMIFGAIALVALLGFLGDFRPNMGQV
VKNGIPQDADGMRKLSWVOMLMSVWOMLMSLGSITPMLKTFDAGKIGVTFHIGKFWVHSFI
ALVLAFGISWMADTMFAHTPQMKALGDTIVMLLTFVHSNQFAAASA
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LPGCLGIVTSCIGYFIMAGSYL"
4469..4657
<gene="Cj0672"
<note="Cj0672, possible periplasmic protein, len: 62 aa;
no HP match. Contains possible N-terminal signal sequence
and second hydrophobic domain".
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4667..6410
<gene="kdpa"
<note="kdpa"
<gene="kdpc"
<note="3..6 1..36"
<EC_number="3..6 1..36"
<note="Cj0676, kdpa, probable potassium-transporting ATPase A chain (EC
0017676, kdpc, probable potassium-transporting ATPase A chain (EC
0017677) is a pseudogene"
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chain)".
5521..5529
<note="G19"
6371..8416
<gene="kdpa"

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"gene="kdpB"
"EC-number=""3.6.1.36"
"note="Cj0677, kdpB, probable potassium-transporting
ATPase B chain, len: 681 aa; similar to e.g. AtpB_ECOLI
potassium-transporting ATPase B chain (EC_3.6.1.36) (682
aa), fasta scores: opt: 2419 z-score: 2798.9 E): 0, 56.6%
identity in 678 aa overlap. No HP match. Contains R300154
EL1-E2 ATPases Phosphorylation site and Pfam match to entry
PF00112 EL1-E2_ATPases. Note that kdpA (Cj0676) and
kdpC (Cj0678) are pseudogenes"
"codon_start="1

```

Query Match: 15.4%; Score: 111.8; DB: 1; Length: 317511; Best Local Similarity: 74.4%; Pred. No.: 1.9e-09; Matches: 154; Conservative: 0; Mismatches: 52; Indels: 1; Gaps: 1